

SEQUENCE LISTING

RECEIVED

JAN 02 2001

RECEIVED 100/200

<110> Meyer, Thomas
Haas, Rainer
Zhengxin, Yan
Gomez-Duarte, Oscar
Lucas, Bernadette



<120> Helicobacter pylori live vaccine

<130> 100564-09008

<140> 09/284,233

<141> 1999-07-28

<150> PCT/EP97/04744

<151> 1997-09-01

<150> EP/96 116 337.5

<151> 1996-10-11

<160> 9

<170> PatentIn version 3.0

<210> 1

<211> 1557

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(1554)

<400> 1

atg	aca	caa	tct	caa	aaa	gta	aga	ttc	tta	gcc	cct	tta	agc	cta	gcg	48
Met	Thr	Gln	Ser	Gln	Lys	Val	Arg	Phe	Leu	Ala	Pro	Leu	Ser	Leu	Ala	
1				5					10					15		

tta	agc	ttg	agc	ttc	aat	cca	gtg	ggc	gct	gaa	gaa	gat	ggg	ggc	ttt	96
Leu	Ser	Leu	Ser	Phe	Asn	Pro	Val	Gly	Ala	Glu	Glu	Asp	Gly	Gly	Phe	
			20					25					30			

atg	acc	ttt	ggg	tat	gaa	tta	ggt	cag	gtg	gtc	caa	caa	gtg	aaa	aac	144
Met	Thr	Phe	Gly	Tyr	Glu	Leu	Gly	Gln	Val	Val	Gln	Gln	Val	Lys	Asn	
		35					40					45				

ccg	ggt	aaa	atc	aaa	gcc	gaa	gaa	tta	gcc	ggc	ttg	tta	aac	tct	acc	192
Pro	Gly	Lys	Ile	Lys	Ala	Glu	Glu	Leu	Ala	Gly	Leu	Leu	Asn	Ser	Thr	
	50					55					60					

aca	aca	aac	aac	acc	aat	atc	aat	att	gca	ggc	aca	gga	ggc	aat	gtc	240
Thr	Thr	Asn	Asn	Thr	Asn	Ile	Asn	Ile	Ala	Gly	Thr	Gly	Gly	Asn	Val	
65						70				75					80	

gcc	ggg	act	ttg	ggc	aac	ctt	ttt	atg	aac	caa	tta	ggc	aat	ttg	att	288
Ala	Gly	Thr	Leu	Gly	Asn	Leu	Phe	Met	Asn	Gln	Leu	Gly	Asn	Leu	Ile	
				85					90					95		

gat	ttg	tat	ccc	act	ttg	aac	act	agt	aat	atc	aca	caa	tgt	ggc	act	336
Asp	Leu	Tyr	Pro	Thr	Leu	Asn	Thr	Ser	Asn	Ile	Thr	Gln	Cys	Gly	Thr	
			100					105					110			

act	aat	agt	ggt	agt	agt	agt	agt	ggt	ggt	ggt	gcg	gcc	aca	gcc	gct	384
Thr	Asn	Ser	Gly	Ser	Ser	Ser	Ser	Gly	Gly	Gly	Ala	Ala	Thr	Ala	Ala	
		115					120					125				

gct	act	act	agc	aat	aag	cct	tgt	ttc	caa	ggt	aac	ctg	gat	ctt	tat	432
Ala	Thr	Thr	Ser	Asn	Lys	Pro	Cys	Phe	Gln	Gly	Asn	Leu	Asp	Leu	Tyr	
	130					135					140					

aga	aaa	atg	gtt	gac	tct	atc	aaa	act	ttg	agt	caa	aac	atc	agc	aag	480
Arg	Lys	Met	Val	Asp	Ser	Ile	Lys	Thr	Leu	Ser	Gln	Asn	Ile	Ser	Lys	
145					150					155					160	

aat	atc	ttt	caa	ggc	aac	aac	aac	acc	acg	agc	caa	aat	ctc	tcc	aac	528
Asn	Ile	Phe	Gln	Gly	Asn	Asn	Asn	Thr	Thr	Ser	Gln	Asn	Leu	Ser	Asn	
			165					170						175		

cag	ctc	agt	gag	ctt	aac	acc	gct	agc	gtt	tat	ttg	act	tac	atg	aac	576
Gln	Leu	Ser	Glu	Leu	Asn	Thr	Ala	Ser	Val	Tyr	Leu	Thr	Tyr	Met	Asn	
			180					185					190			

tcg	ttc	tta	aac	gcc	aat	aac	caa	gcg	ggt	ggg	att	ttt	caa	aac	aac	624
Ser	Phe	Leu	Asn	Ala	Asn	Asn	Gln	Ala	Gly	Gly	Ile	Phe	Gln	Asn	Asn	
		195					200					205				

act aat caa gct tat gga aat ggg gtt acc gct caa caa atc gct tat Thr Asn Gln Ala Tyr Gly Asn Gly Val Thr Ala Gln Gln Ile Ala Tyr 210 215 220	672
atc cta aag caa gct tca atc act atg ggg cca agc ggt gat agc ggt Ile Leu Lys Gln Ala Ser Ile Thr Met Gly Pro Ser Gly Asp Ser Gly 225 230 235 240	720
gct gcc gca gcg ttt ttg gat gcc gct tta gcg caa cat gtt ttc aac Ala Ala Ala Ala Phe Leu Asp Ala Ala Leu Ala Gln His Val Phe Asn 245 250 255	768
tcc gct aac gcc ggg aac gat ttg agc gct aag gaa ttc act agc ttg Ser Ala Asn Ala Gly Asn Asp Leu Ser Ala Lys Glu Phe Thr Ser Leu 260 265 270	816
gtg caa aat atc gtc aat aat tct caa aac gct tta acg cta gcc aac Val Gln Asn Ile Val Asn Asn Ser Gln Asn Ala Leu Thr Leu Ala Asn 275 280 285	864
aac gct aac atc agc aat tca aca ggc tat caa gtg agc tat ggc ggg Asn Ala Asn Ile Ser Asn Ser Thr Gly Tyr Gln Val Ser Tyr Gly Gly 290 295 300	912
aat att gat caa gcg cga tct acc caa cta tta aac aac acc aca aac Asn Ile Asp Gln Ala Arg Ser Thr Gln Leu Leu Asn Asn Thr Thr Asn 305 310 315 320	960
act ttg gct aaa gtt agc gct ttg aat aac gag ctt aaa gct aac cca Thr Leu Ala Lys Val Ser Ala Leu Asn Asn Glu Leu Lys Ala Asn Pro 325 330 335	1008
tgg ctt ggg aat ttt gcc gcc ggt aac agc tct caa gtg aat gcg ttt Trp Leu Gly Asn Phe Ala Ala Gly Asn Ser Ser Gln Val Asn Ala Phe 340 345 350	1056
aac ggg ttt atc act aaa atc ggt tac aag caa ttc ttt ggg gaa aac Asn Gly Phe Ile Thr Lys Ile Gly Tyr Lys Gln Phe Phe Gly Glu Asn 355 360 365	1104
aag aat gtg ggc tta cgc tac tac ggc ttc ttc agc tat aac ggc gcg Lys Asn Val Gly Leu Arg Tyr Tyr Gly Phe Phe Ser Tyr Asn Gly Ala 370 375 380	1152
ggc gtg ggt aat ggc cct act tac aat caa gtc aat ttg ctc act tat Gly Val Gly Asn Gly Pro Thr Tyr Asn Gln Val Asn Leu Leu Thr Tyr 385 390 395 400	1200
ggg gtg ggg act gat gtg ctt tac aat gtg ttt agc cgc tct ttt ggt Gly Val Gly Thr Asp Val Leu Tyr Asn Val Phe Ser Arg Ser Phe Gly 405 410 415	1248
agt agg agt ctt aat gcg ggc ttc ttt ggg ggg atc caa ctc gca ggg Ser Arg Ser Leu Asn Ala Gly Phe Phe Gly Gly Ile Gln Leu Ala Gly 420 425 430	1296
gat act tac atc agc acg cta aga aac agc tct cag ctt gcg agc aga Asp Thr Tyr Ile Ser Thr Leu Arg Asn Ser Ser Gln Leu Ala Ser Arg 435 440 445	1344

cct aca gcg acg aaa ttc caa ttc ttg ttt gat gtg ggc tta cgc atg 1392
 Pro Thr Ala Thr Lys Phe Gln Phe Leu Phe Asp Val Gly Leu Arg Met
 450 455 460

aac ttt ggt atc ttg aaa aaa gac ttg aaa agc cat aac cag cat tct 1440
 Asn Phe Gly Ile Leu Lys Lys Asp Leu Lys Ser His Asn Gln His Ser
 465 470 475 480

ata gaa atc ggt gtg caa atc cct acg att tac aac act tac tat aaa 1488
 Ile Glu Ile Gly Val Gln Ile Pro Thr Ile Tyr Asn Thr Tyr Tyr Lys
 485 490 495

gct ggc ggt gct gaa gtg aaa tac ttc cgc cct tat agc gtg tat tgg 1536
 Ala Gly Gly Ala Glu Val Lys Tyr Phe Arg Pro Tyr Ser Val Tyr Trp
 500 505 510

gtc tat ggc tac gcc ttc taa 1557
 Val Tyr Gly Tyr Ala Phe
 515

<210> 2

<211> 518

<212> PRT

<213> Helicobacter pylori

<400> 2

Met Thr Gln Ser Gln Lys Val Arg Phe Leu Ala Pro Leu Ser Leu Ala
 1 5 10 15

Leu Ser Leu Ser Phe Asn Pro Val Gly Ala Glu Glu Asp Gly Gly Phe
 20 25 30

Met Thr Phe Gly Tyr Glu Leu Gly Gln Val Val Gln Gln Val Lys Asn
 35 40 45

Pro Gly Lys Ile Lys Ala Glu Glu Leu Ala Gly Leu Leu Asn Ser Thr
 50 55 60

Thr Thr Asn Asn Thr Asn Ile Asn Ile Ala Gly Thr Gly Gly Asn Val
 65 70 75 80

Ala Gly Thr Leu Gly Asn Leu Phe Met Asn Gln Leu Gly Asn Leu Ile
 85 90 95

Asp Leu Tyr Pro Thr Leu Asn Thr Ser Asn Ile Thr Gln Cys Gly Thr
 100 105 110

Thr Asn Ser Gly Ser Ser Ser Ser Gly Gly Gly Ala Ala Thr Ala Ala
 115 120 125

Ala Thr Thr Ser Asn Lys Pro Cys Phe Gln Gly Asn Leu Asp Leu Tyr
 130 135 140

Arg Lys Met Val Asp Ser Ile Lys Thr Leu Ser Gln Asn Ile Ser Lys
 145 150 155 160

Asn Ile Phe Gln Gly Asn Asn Asn Thr Thr Ser Gln Asn Leu Ser Asn
 165 170 175

Gln Leu Ser Glu Leu Asn Thr Ala Ser Val Tyr Leu Thr Tyr Met Asn
 180 185 190

Ser Phe Leu Asn Ala Asn Asn Gln Ala Gly Gly Ile Phe Gln Asn Asn
 195 200 205

Thr Asn Gln Ala Tyr Gly Asn Gly Val Thr Ala Gln Gln Ile Ala Tyr
 210 215 220

Ile Leu Lys Gln Ala Ser Ile Thr Met Gly Pro Ser Gly Asp Ser Gly
 225 230 235 240

Ala Ala Ala Ala Phe Leu Asp Ala Ala Leu Ala Gln His Val Phe Asn
 245 250 255

Ser Ala Asn Ala Gly Asn Asp Leu Ser Ala Lys Glu Phe Thr Ser Leu
 260 265 270

Val Gln Asn Ile Val Asn Asn Ser Gln Asn Ala Leu Thr Leu Ala Asn
 275 280 285

Asn Ala Asn Ile Ser Asn Ser Thr Gly Tyr Gln Val Ser Tyr Gly Gly
 290 295 300

Asn Ile Asp Gln Ala Arg Ser Thr Gln Leu Leu Asn Asn Thr Thr Asn
 305 310 315 320

Thr Leu Ala Lys Val Ser Ala Leu Asn Asn Glu Leu Lys Ala Asn Pro
 325 330 335

Trp Leu Gly Asn Phe Ala Ala Gly Asn Ser Ser Gln Val Asn Ala Phe
 340 345 350

Asn Gly Phe Ile Thr Lys Ile Gly Tyr Lys Gln Phe Phe Gly Glu Asn
355 360 365

Lys Asn Val Gly Leu Arg Tyr Tyr Gly Phe Phe Ser Tyr Asn Gly Ala
370 375 380

Gly Val Gly Asn Gly Pro Thr Tyr Asn Gln Val Asn Leu Leu Thr Tyr
385 390 395 400

Gly Val Gly Thr Asp Val Leu Tyr Asn Val Phe Ser Arg Ser Phe Gly
405 410 415

Ser Arg Ser Leu Asn Ala Gly Phe Phe Gly Gly Ile Gln Leu Ala Gly
420 425 430

Asp Thr Tyr Ile Ser Thr Leu Arg Asn Ser Ser Gln Leu Ala Ser Arg
435 440 445

Pro Thr Ala Thr Lys Phe Gln Phe Leu Phe Asp Val Gly Leu Arg Met
450 455 460

Asn Phe Gly Ile Leu Lys Lys Asp Leu Lys Ser His Asn Gln His Ser
465 470 475 480

Ile Glu Ile Gly Val Gln Ile Pro Thr Ile Tyr Asn Thr Tyr Tyr Lys
485 490 495

Ala Gly Gly Ala Glu Val Lys Tyr Phe Arg Pro Tyr Ser Val Tyr Trp
500 505 510

Val Tyr Gly Tyr Ala Phe
515

<210> 3

<211> 1557

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(1554)

<400> 3

atg ata aaa aag aat aga acg ctg ttt ctt agt cta gcc ctt tgc gct Met Ile Lys Lys Asn Arg Thr Leu Phe Leu Ser Leu Ala Leu Cys Ala 1 5 10 15	48
agc ata agt tat gcc gaa gat gat gga ggg ttt ttc acc gtc ggt tat Ser Ile Ser Tyr Ala Glu Asp Asp Gly Gly Phe Phe Thr Val Gly Tyr 20 25 30	96
cag ctc ggg caa gtc atg caa gat gtc caa aac cca ggc ggc gct aaa Gln Leu Gly Gln Val Met Gln Asp Val Gln Asn Pro Gly Ala Lys 35 40 45	144
agc gac gaa ctc gcc aga gag ctt aac gct gat gta acg aac aac att Ser Asp Glu Leu Ala Arg Glu Leu Asn Ala Asp Val Thr Asn Asn Ile 50 55 60	192
tta aac aac aac acc gga ggc aac atc gca ggg gcg ttg agt aac gct Leu Asn Asn Asn Thr Gly Gly Asn Ile Ala Gly Ala Leu Ser Asn Ala 65 70 75 80	240
ttc tcc caa tac ctt tat tgc ctt tta ggg gct tac ccc aca aaa ctc Phe Ser Gln Tyr Leu Tyr Ser Leu Leu Gly Ala Tyr Pro Thr Lys Leu 85 90 95	288
aat ggt agc gat gtg tct gcg aac gct ctt tta agt ggt gcg gta ggc Asn Gly Ser Asp Val Ser Ala Asn Ala Leu Leu Ser Gly Ala Val Gly 100 105 110	336
tct ggg act tgt gcg gct gca ggg acg gct ggt ggc act tct ctt aac Ser Gly Thr Cys Ala Ala Ala Gly Thr Ala Gly Gly Thr Ser Leu Asn 115 120 125	384
act caa agc act tgc acc gtt gcg ggc tat tac tgg ctc cct agc ttg Thr Gln Ser Thr Cys Thr Val Ala Gly Tyr Tyr Trp Leu Pro Ser Leu 130 135 140	432
act gac agg att tta agc acg atc ggc agc cag act aac tac ggc acg Thr Asp Arg Ile Leu Ser Thr Ile Gly Ser Gln Thr Asn Tyr Gly Thr 145 150 155 160	480
aac acc aat ttc ccc aac atg caa caa cag ctc acc tac ttg aat gcg Asn Thr Asn Phe Pro Asn Met Gln Gln Gln Leu Thr Tyr Leu Asn Ala 165 170 175	528
ggg aat gtg ttt ttt aat gcg atg aat aag gct tta gag aat aag aat Gly Asn Val Phe Phe Asn Ala Met Asn Lys Ala Leu Glu Asn Lys Asn 180 185 190	576
gga act agt agt gct agt gga act agt ggt gcg act ggt tca gat ggt Gly Thr Ser Ser Ala Ser Gly Thr Ser Gly Ala Thr Gly Ser Asp Gly 195 200 205	624
caa act tac tcc aca caa gct atc caa tac ctt caa ggc caa caa aat Gln Thr Tyr Ser Thr Gln Ala Ile Gln Tyr Leu Gln Gly Gln Gln Asn 210 215 220	672

atc tta aat aac gca gcg aac ttg ctc aag caa gat gaa ttg ctc tta Ile Leu Asn Asn Ala Ala Asn Leu Leu Lys Gln Asp Glu Leu Leu Leu 225 230 235 240	720
gaa gct ttc aac tct gcc gta gcc gcc aac att ggg aat aag gaa ttc Glu Ala Phe Asn Ser Ala Val Ala Ala Asn Ile Gly Asn Lys Glu Phe 245 250 255	768
aat tca gcc gct ttt aca ggt ttg gtg caa ggc att att gat caa tct Asn Ser Ala Ala Phe Thr Gly Leu Val Gln Gly Ile Ile Asp Gln Ser 260 265 270	816
caa gcg gtt tat aac gag ctc act aaa aac acc att agc ggg agt gcg Gln Ala Val Tyr Asn Glu Leu Thr Lys Asn Thr Ile Ser Gly Ser Ala 275 280 285	864
gtt att agc gct ggg ata aac tcc aac caa gct aac gct gtg caa ggg Val Ile Ser Ala Gly Ile Asn Ser Asn Gln Ala Asn Ala Val Gln Gly 290 295 300	912
cgc gct agt cag ctc cct aac gct ctt tat aac gcg caa gta act ttg Arg Ala Ser Gln Leu Pro Asn Ala Leu Tyr Asn Ala Gln Val Thr Leu 305 310 315 320	960
gat aaa atc aat gcg ctc aat aat caa gtg aga agc atg cct tac ttg Asp Lys Ile Asn Ala Leu Asn Asn Gln Val Arg Ser Met Pro Tyr Leu 325 330 335	1008
ccc caa ttc aga gcc ggg aac agc cgt tca acg aat att tta aac ggg Pro Gln Phe Arg Ala Gly Asn Ser Arg Ser Thr Asn Ile Leu Asn Gly 340 345 350	1056
ttt tac acc aaa ata ggc tat aag caa ttc ttc ggg aag aaa agg aat Phe Tyr Thr Lys Ile Gly Tyr Lys Gln Phe Phe Gly Lys Lys Arg Asn 355 360 365	1104
atc ggt ttg cgc tat tat ggt ttc ttt tct tat aac gga gcg agc gtg Ile Gly Leu Arg Tyr Tyr Gly Phe Phe Ser Tyr Asn Gly Ala Ser Val 370 375 380	1152
ggc ttt aga tcc act caa aat aat gta ggg tta tac act tat ggg gtg Gly Phe Arg Ser Thr Gln Asn Asn Val Gly Leu Tyr Thr Tyr Gly Val 385 390 395 400	1200
ggg act gat gtg ttg tat aac atc ttt agc cgc tcc tat caa aac cgc Gly Thr Asp Val Leu Tyr Asn Ile Phe Ser Arg Ser Tyr Gln Asn Arg 405 410 415	1248
tct gtg gat atg ggc ttt ttt agc ggt atc caa tta gcc ggt gag acc Ser Val Asp Met Gly Phe Phe Ser Gly Ile Gln Leu Ala Gly Glu Thr 420 425 430	1296
ttc caa tcc acg ctc aga gat gac ccc aat gtg aaa ttg cat ggg aaa Phe Gln Ser Thr Leu Arg Asp Asp Pro Asn Val Lys Leu His Gly Lys 435 440 445	1344
atc aat aac acg cac ttc cag ttc ctc ttt gac ttc ggt atg agg atg Ile Asn Asn Thr His Phe Gln Phe Leu Phe Asp Phe Gly Met Arg Met 450 455 460	1392

aac ttc ggt aag ttg gac ggg aaa tcc aac cgc cac aac cag cac acg 1440
Asn Phe Gly Lys Leu Asp Gly Lys Ser Asn Arg His Asn Gln His Thr
465 470 475 480

tca gca ggg act acc gtg aag tat ttc cgt cct tat agc gtt tat tgg 1536
Ser Ala Gly Thr Thr Val Lys Tyr Phe Arg Pro Tyr Ser Val Tyr Trp
500 505 510

<210> 4

<400> 4

Thr Gln Ser Thr Cys Thr Val Ala Gly Tyr Tyr Trp Leu Pro Ser Leu
 130 135 140

Thr Asp Arg Ile Leu Ser Thr Ile Gly Ser Gln Thr Asn Tyr Gly Thr
 145 150 155 160

Asn Thr Asn Phe Pro Asn Met Gln Gln Gln Leu Thr Tyr Leu Asn Ala
 165 170 175

Gly Asn Val Phe Phe Asn Ala Met Asn Lys Ala Leu Glu Asn Lys Asn
 180 185 190

Gly Thr Ser Ser Ala Ser Gly Thr Ser Gly Ala Thr Gly Ser Asp Gly
 195 200 205

Gln Thr Tyr Ser Thr Gln Ala Ile Gln Tyr Leu Gln Gly Gln Gln Asn
 210 215 220

Ile Leu Asn Asn Ala Ala Asn Leu Leu Lys Gln Asp Glu Leu Leu Leu
 225 230 235 240

Glu Ala Phe Asn Ser Ala Val Ala Ala Asn Ile Gly Asn Lys Glu Phe
 245 250 255

Asn Ser Ala Ala Phe Thr Gly Leu Val Gln Gly Ile Ile Asp Gln Ser
 260 265 270

Gln Ala Val Tyr Asn Glu Leu Thr Lys Asn Thr Ile Ser Gly Ser Ala
 275 280 285

Val Ile Ser Ala Gly Ile Asn Ser Asn Gln Ala Asn Ala Val Gln Gly
 290 295 300

Arg Ala Ser Gln Leu Pro Asn Ala Leu Tyr Asn Ala Gln Val Thr Leu
 305 310 315 320

Asp Lys Ile Asn Ala Leu Asn Asn Gln Val Arg Ser Met Pro Tyr Leu
 325 330 335

Pro Gln Phe Arg Ala Gly Asn Ser Arg Ser Thr Asn Ile Leu Asn Gly
 340 345 350

Phe Tyr Thr Lys Ile Gly Tyr Lys Gln Phe Phe Gly Lys Lys Arg Asn
 355 360 365

Ile Gly Leu Arg Tyr Tyr Gly Phe Phe Ser Tyr Asn Gly Ala Ser Val
370 375 380

Gly Phe Arg Ser Thr Gln Asn Asn Val Gly Leu Tyr Thr Tyr Gly Val
385 390 395 400

Gly Thr Asp Val Leu Tyr Asn Ile Phe Ser Arg Ser Tyr Gln Asn Arg
405 410 415

Ser Val Asp Met Gly Phe Phe Ser Gly Ile Gln Leu Ala Gly Glu Thr
420 425 430

Phe Gln Ser Thr Leu Arg Asp Asp Pro Asn Val Lys Leu His Gly Lys
435 440 445

Ile Asn Asn Thr His Phe Gln Phe Leu Phe Asp Phe Gly Met Arg Met
450 455 460

Asn Phe Gly Lys Leu Asp Gly Lys Ser Asn Arg His Asn Gln His Thr
465 470 475 480

Val Glu Phe Gly Val Val Val Pro Thr Ile Tyr Asn Thr Tyr Tyr Lys
485 490 495

Ser Ala Gly Thr Thr Val Lys Tyr Phe Arg Pro Tyr Ser Val Tyr Trp
500 505 510

Ser Tyr Gly Tyr Ser Phe
515

<210> 5

<211> 656

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (567)..(656)

<400> 5
agatctatga atctatgata tcaacactct ttttgataaa ttttctcgag gtaccgagct 60
tgaggcatca aataaaacga aaggctcagt cgaaagactg ggcctttcgt tttatctggt 120
gtttgtcggg gaacgctctc ctgagtagga caaatccgcc gggagcggat ttgaacggtg 180
cgaagcaacg gcccggaggg tggcgggcag gacgcccgcc ataaactgcc acaagctcgg 240
taccgttgat cttcctatgg tgcactctca gtacaatctg ctctgatgcg ctacgtgact 300
gggtcatggc tgcgccccga caccgcgcaa caccgctga cgcgcctga cgggcttgtc 360
tgctcccggc atccgcttac agacaagctg tgaccgtctc cgggagctgc atgtgtcaga 420
ggttttcacc gtcatcaccg aaacgcgcga ggcccagcgc ttcgaacttc tgatagactt 480
cgaaattaat acgactcact ataggagagac cacaacggtt tccctctaga aataattttg 540
tttaacttta agaaggagat atacat atg aaa ctg act ccc aaa gag tta gac 593
Met Lys Leu Thr Pro Lys Glu Leu Asp
1 5
aag ttg atg ctc cac tac gct gga gaa ttg gct aaa aaa cgc aaa gaa 641
Lys Leu Met Leu His Tyr Ala Gly Glu Leu Ala Lys Lys Arg Lys Glu
10 15 20 25
aaa ggc att aag ctt 656
Lys Gly Ile Lys Leu
30

<210> 6

<211> 30

<212> PRT

<213> Helicobacter pylori

<400> 6

Met Lys Leu Thr Pro Lys Glu Leu Asp Lys Leu Met Leu His Tyr Ala
1 5 10 15
Gly Glu Leu Ala Lys Lys Arg Lys Glu Lys Gly Ile Lys Leu
20 25 30

<210> 7

<211> 656

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (567)..(656)

<400> 7

agatctatga atctatgata tcaacactct ttttgataaa ttttctcgag gtaccgagct 60

tgaggcatca aataaaacga aaggctcagt cgaaagactg ggcctttcgt tttatctggt 120

gtttgtcggg gaacgctctc ctgagtagga caaatccgcc gggagcggat ttgaacgttg 180

cgaagcaacg gcccggaggg tggcgggcag gacgcccgcc ataaactgcc acaagctcgg 240

taccgttgat cttcctatgg tgcactctca gtacaatctg ctctgatgcg ctacgtgact 300

gggtcatggc tgcgccccga caccgcgcaa caccgctga cgcgccctga cgggcttgtc 360

tgctcccggc atccgcttac agacaagctg tgaccgtctc cgggagctgc atgtgtcaga 420

ggttttcacc gtcacacccg aaacgcgcga ggcccagcgc ttcgaccttc tgatagactt 480

cgaaattaat acgactcact atagggagac cacaacgggt tccctctaga aataattttg 540

tttaacttta agaaggagat atacat atg aaa ctg act ccc aaa gag tta gac 593
Met Lys Leu Thr Pro Lys Glu Leu Asp
1 5

agg ttg atg ctc cac tac gct gga gaa ttg gct aaa aaa cgc aaa gaa 641
Arg Leu Met Leu His Tyr Ala Gly Glu Leu Ala Lys Lys Arg Lys Glu
10 15 20 25

aaa ggc att aag ctt 656
Lys Gly Ile Lys Leu
30

<210> 8

<211> 31

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(31)

<223> Primer YZ019

<400> 8
ggaattccat atgaaactga ctcccaaaga g

31

<210> 9

<211> 27

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(27)

<223> Primer RH132

<400> 9
ctgcagtcga ctagaaaatg ctaagag

27